

OIKE

## RAW SEQUENCE LISTING

DATE: 04/04/2001

PATENT APPLICATION: US/09/809,545

TIME: 14:11:29

Input Set : A:\SCIOS17ASEQ.TXT

Output Set: N:\CRF3\04042001\I809545.raw

4 <110> APPLICANT: Stanton, Lawrence W.  
5 White, R. Tyler  
8 <120> TITLE OF INVENTION: SECRETED FACTORS  
11 <130> FILE REFERENCE: SCIOS.017A  
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/809,545  
C--> 13 <141> CURRENT FILING DATE: 2001-03-14  
13 <150> PRIOR APPLICATION NUMBER: US 60/193,548  
14 <151> PRIOR FILING DATE: 2000-03-31  
16 <160> NUMBER OF SEQ ID NOS: 70 84 (include skipped sequences in response)  
18 <170> SOFTWARE: FastSEQ for Windows Version 4.0

Does Not Comply  
Corrected Diskette Needed

## ERRORED SEQUENCES

E--> 1469 <210> SEQ ID NO: 31  
E--> 1516 <210> SEQ ID NO: 33  
E--> 1825 <210> SEQ ID NO: 40  
E--> 2780 <210> SEQ ID NO: 65  
E--> 2810 <210> SEQ ID NO: 69  
E--> 2825 <210> SEQ ID NO: 71  
E--> 2842 <210> SEQ ID NO: 74  
E--> 2865 <210> SEQ ID NO: 76

See following pages (2-3,5-10)

fyi

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

1809,545

2

<400> 29

tctagcgaac cccttcgcag aaacccaaag ttacagacca gaccctaccc aacatccagt 60  
cagcaatcca gctggagaaa cgcttgag atg aca agg gac ttt cag aag caa 112

Met Thr Arg Asp Phe Gln Lys Gln  
1 5

gcc ttg ata aga cag gaa aag cag aat tct aat aaa gat atg agg aaa 160  
Ala Leu Ile Arg Gln Glu Lys Gln Asn Ser Asn Lys Asp Met Arg Lys  
10 15 20

aat gac atg ggc ctt caa cct ctg cct gta ggg aag gac gca cac agt 208  
Asn Asp Met Gly Leu Gln Pro Leu Pro Val Gly Lys Asp Ala His Ser  
25 30 35 40

gca cca gga gtg aca gtc tct ggg aaa aac cac aaa aga act cag gca 256  
Ala Pro Gly Val Thr Val Ser Gly Lys Asn His Lys Arg Thr Gln Ala  
45 50 55

cct gac aag aaa cag aga att gat gtt tgt cta gaa agc cag gac ttt 304  
Pro Asp Lys Lys Gln Arg Ile Asp Val Cys Leu Glu Ser Gln Asp Phe  
60 65 70

cta atg aag aca aat act tcc aag gag tta aaa atg gca atg gag agg 352  
Leu Met Lys Thr Asn Thr Ser Lys Glu Leu Lys Met Ala Met Glu Arg  
75 80 85

tcc ttt aat cca gtc aac ctt tcc ctg act gtg gtg taa aagaaaatga 401  
Ser Phe Asn Pro Val Asn Leu Ser Leu Thr Val Val \*  
90 95 100

ggagcgcctt ctctccatct tcccctcctt cttctccttc caattgcgtc atctgaaatt 461  
gaatttcctc tccctcctcca ccacctataa tgctgtgcct gaaaaaatg agtttctctc 521  
ctcatcacc acagagaagt caagggctga acttgagagc ctccaaccc tgcctcttcc 581  
tccaccacca ggagatgaga aatctgatca ggaatgtcta ccaacatccc tacctcctcc 641  
ccctcccaca gctccatccc aaccagcaca tcttctttcc tccctctgttc tagaacatca 701  
cagtgaagca tttttacaac agtattcccg aaaagaaacc ttggactctc atcggttca 761  
ctcacaggct aaaatcctaa caggaaaatc accaccccca aactcctcca aacccaaact 821  
tcccgagaga atcaaagcta agatgagcca ggattcacca agcgggtgaat tggaaagatc 881  
tctgtcagat gtggaaatta aaactaccct ctcaaaggat cagaaaagtt cgctggtggc 941  
agaaagccgt gagcacacag aggccaaagca agaagtattc cgaaaaagcc ttggaagaaa 1001  
acagctgtcc attagctctg caaactccct ctctcagaca gttccagaaa tcccagcacc 1061  
caaggaaaaa cagacagcac cccttggttaa atctcactca tcccatcag gttcagaaca 1121  
acaaagtcct aagccttaca tgagaaaatt taagacaccc ttaatgattg cggaagaaaa 1181  
atacagacaa caaagggag agcttgagaa acagagacgg gagagttctt gccatagcat 1241  
catcaaaaca gaaaccagc accgcagctt atcaaanntt aaaaaaaaaa aaannnagc 1301  
ggncgccc 1310

<210> 31

→ Sequence 30 missing

Please account for these missing sequences.

09/809545

3

&lt;400&gt; 31

tctagcgaac	cccttcgctt	tttttttttt	tttttttttt	ttttccccc	tttcctat	60
attaatggg	ggaagtatgt	ttatgtgga	tttatccact	tcttttagat	tctcctacct	120
gttgatctgt	aattattcct	agtagtctct	tagagttctt	agaagcatgc	tgttaccgct	180
aatatttcct	tttggtttgg	atcttactta	aacatattgt	ttccttactc	tctttttcat	240
cccagcttgt	ctaactgaaa	ggccagaccc	aacttgatct	atccctttaa	aacttc atg	299

Met

1

tct	tgg	cct	ggt	gat	ttc	tct	gct	cca	ggt	gtc	acc	gaa	ggg	ggt	cgc	347
Ser	Trp	Pro	Val	Asp	Phe	Ser	Ala	Pro	Gly	Val	Thr	Glu	Gly	Val	Arg	
		5						10					15			

cta	gcg	aac	ccc	ttc	gta	aca	gcc	aag	ggt	ttt	gag	aca	gag	ggt	tca	395
Leu	Ala	Asn	Pro	Phe	Val	Thr	Ala	Lys	Val	Phe	Glu	Thr	Glu	Val	Ser	
		20					25					30				

aca	gca	ttc	ctg	gag	gag	aca	caa	agg	aca	gat	gag	tca	cat	gaa	gga	443
Thr	Ala	Phe	Leu	Glu	Glu	Thr	Gln	Arg	Thr	Asp	Glu	Ser	His	Glu	Gly	
		35				40					45					

tgg	gag	gag	gga	agg	tgg	ctg	ttg	ata	ggt	att	ttg	aga	cac	tct	att	491
Trp	Glu	Glu	Gly	Arg	Trp	Leu	Leu	Ile	Gly	Ile	Leu	Arg	His	Ser	Ile	
	50				55				60					65		

tga	gtcctacaca	acactccccc	ctccccccaa	accattttta	tgtctattga	544
-----	------------	------------	------------	------------	------------	-----

\*

cctttcctct	agtcatacag	ggaaattcac	agttacctac	aaagaaccac	taattgtaac	604
aagtcaagag	gaaacttatt	tttgataatg	actcattgaa	gatgttttga	aaatttaaaa	664
ataagctctg	ttagcagaag	tctgttngaa	aagcangaag	gaantgtttg	tttattanat	724
aaataaaaagg	cggcgaggac	aacaaaaaaa	aaaaaaaaaa	aagcggccgc		774

&lt;210&gt; 33

→ Sequence 32  
missing

all next page

&lt;400&gt; 38

tctagcgaac cccttcgga accccttcgc tgcatactca taaagctacc tcaagacaga 60  
 gcgtaactgc ctcattctag gactggactc ggggaagaca gcagacacac catcagggag 120  
 cccttggtta tctccagaac atg gca agc cgt gga tac ctg cat cac ctg ctg 173  
 Met Ala Ser Arg Gly Tyr Leu His His Leu Leu  
 1 5 10

act gca gag gga gcc tgg gag gag ttt gta tca aag gcc aag ttg ccc 221  
 Thr Ala Glu Gly Ala Trp Glu Glu Phe Val Ser Lys Ala Lys Leu Pro  
 15 20 25

agg gat agg gca gtg gcc ctc cac aaa gca ctg agg gat ctg aca gca 269  
 Arg Asp Arg Ala Val Ala Leu His Lys Ala Leu Arg Asp Leu Thr Ala  
 30 35 40

ctc ttg gcc ata gca gaa aga ggc aga tct cgg aaa ggc tgg aaa ggc 317  
 Leu Leu Ala Ile Ala Glu Arg Gly Arg Ser Arg Lys Gly Trp Lys Gly  
 45 50 55

aag gag aag ttt gtg aaa gca ttt cct tgc ttg aaa gca gac ttg gag 365  
 Lys Glu Lys Phe Val Lys Ala Phe Pro Cys Leu Lys Ala Asp Leu Glu  
 60 65 70 75

gag cac atc agc cag ctc tat gcc cta gcc gac cat gct gag gaa ctg 413  
 Glu His Ile Ser Gln Leu Tyr Ala Leu Ala Asp His Ala Glu Glu Leu  
 80 85 90

cac agg ggc tgc acc gtc tcc aac atg gtg gct gac tcc ttc agt gtt 461  
 His Arg Gly Cys Thr Val Ser Asn Met Val Ala Asp Ser Phe Ser Val  
 95 100 105

gcc tcc gac atc ctg aac atc ttt ggt ctc ttt ctg gca cct gag tca 509  
 Ala Ser Asp Ile Leu Asn Ile Phe Gly Leu Phe Leu Ala Pro Glu Ser  
 110 115 120

gca gag gga agt ctg gtg ctc tcg gca gca ggc ttg ggg ctg ggg gta 557  
 Ala Glu Gly Ser Leu Val Leu Ser Ala Ala Gly Leu Gly Leu Gly Val  
 125 130 135

gca gct act gtg act aat gtt gct act tca atc atg aag gaa aca agc 605  
 Ala Ala Thr Val Thr Asn Val Ala Thr Ser Ile Met Lys Glu Thr Ser  
 140 145 150 155

agg gtt ttg gat gga gtc gaa gct ggt cac cat ggt tca acc gcc atg 653  
 Arg Val Leu Asp Gly Val Glu Ala Gly His His Gly Ser Thr Ala Met  
 160 165 170

gat ata ctg gag gaa gct ggc aca agt gtg gct agg att gcc agc gag 701  
 Asp Ile Leu Glu Glu Ala Gly Thr Ser Val Ala Arg Ile Ala Ser Glu  
 175 180 185

atc cct cag gct acc aga gat atc acc aga gac ctg gaa gcc ctt gag 749  
 Ile Pro Gln Ala Thr Arg Asp Ile Thr Arg Asp Leu Glu Ala Leu Glu  
 190 195 200

cag cac atg aat gcc ctc agt ctg gtc aga gcc aac cct cgc cta gaa 797  
 Gln His Met Asn Ala Leu Ser Leu Val Arg Ala Asn Pro Arg Leu Glu

09/809,545 S

205	210	215	
gaa gat gcc agg gcc ctc atc aat gca ggt agc atc cct gcc caa cgg			845
Glu Asp Ala Arg Ala Leu Ile Asn Ala Gly Ser Ile Pro Ala Gln Arg			
220	225	230	235
gct aaa cag gtg cgg gcc agt ctg aaa gga acc cct ctg gca atg agc			893
Ala Lys Gln Val Arg Ala Ser Leu Lys Gly Thr Pro Leu Ala Met Ser			
	240	245	250
aag gaa gac cgg atc cgc agt gcc acc acc act ggg gtc acc ctc ttg			941
Lys Glu Asp Arg Ile Arg Ser Ala Thr Thr Thr Gly Val Thr Leu Leu			
	255	260	265
cgt gat gtg ggg agc ctt gtg aac gag tgc aag cag ttg tac gaa ggg			989
Arg Asp Val Gly Ser Leu Val Asn Glu Ser Lys Gln Leu Tyr Glu Gly			
	270	275	280
tct gct tcc gaa tgc gca gca gca cta agg aag ctg gct cag gag ctg			1037
Ser Ala Ser Glu Ser Ala Ala Ala Leu Arg Lys Leu Ala Gln Glu Leu			
	285	290	295
gag gag aag cta ggg gag ctc atg aaa ttc tac gag aca atc tga			1082
Glu Glu Lys Leu Gly Glu Leu Met Lys Phe Tyr Glu Thr Ile *			
300	305	310	
tcagggtttca gccagtcacc ccatcccca gacatgcaga catcanggga gaggatctgg			1142
acagaggttag ggaccatgga ggtgctgtta gaaggagagc aagactacag tcagggtccga			1202
gggacatagt gtggaggcct gtttgatgaa cacarcaggt taraggatgg agcagtggat			1262
caaagtgaga tccactggag cctgagacsa gggaccagag gatgtgctgc aagagggact			1322
gggaaaattg aaatctanac taaacatgga aaaaaggcag tttcgaaaga ctagaaaacc			1382
ctccccatct gagccattgg aaacccacaca aaacacaaac cagagagaaa agtgtgtgct			1442
ctctaaacaa gtcgtggccc ccagttcccc agcccactcc caccctcagg ggtggcatca			1502
aataaattgt ttccatttca aaaaaaaaaa naaanaaaaa aaaagcggcc gc			1554

<210> 40

→ sequence 39 missing

09/809,545 6

<400> 60

Met	Lys	Pro	Glu	Asn	Cys	Phe	Thr	Ile	Thr	Ser	Ser	Phe	Trp	Pro	Ser
1				5					10					15	
Leu	Arg	Pro	Trp	Lys	Ile	Val	Cys	Gly	Asp	Ser	Tyr	Arg	Lys	Gln	Thr
			20					25					30		
Gly	Arg	Leu	Lys	Gln	Thr	Arg	Ser	Lys	Val	Arg	Cys	Arg	Cys	His	Gly
		35					40					45			
Gln	Thr	Leu	Gly	Glu	Ala	Trp	Ala	Thr	Leu	Val	Phe	Met	Leu	Glu	Arg
		50				55					60				
Arg	Arg	Glu	Leu	Leu	Gly	Leu	Thr	Ser	Glu	Phe	Phe	Gln	Ser	Ala	Leu
65					70					75				80	
Glu	Phe	Ala	Ile	Lys	Ile	Asp	Gln	Ala	Glu	Asp	Phe	Leu	Gln	Asn	Pro
				85					90					95	
His	Glu	Phe	Glu	Ser	Ala	Glu	Ala	Leu	Gln	Ser	Leu	Leu	Leu	Leu	His
			100					105					110		
Asp	Arg	His	Ala	Lys	Glu	Leu	Leu	Glu	Arg	Ser	Leu	Val	Leu	Leu	Asn
		115					120					125			
Lys	Ser	Gln	Gln	Leu	Thr	Asp	Phe	Ile	Glu	Lys	Phe	Lys	Cys	Asp	Gly
		130				135					140				
Ser	Pro	Val	Asn	Ser	Glu	Leu	Ile	Gln	Gly	Ala	Gln	Ser	Ser	Cys	Leu
145					150					155					160
Lys	Ile	Asp	Ser	Leu	Leu	Glu	Leu	Leu	Gln	Asp	Arg	Arg	Arg	Gln	Leu
				165					170					175	
Asp	Lys	His	Leu	Gln	Gln	Gln	Arg	Gln	Glu	Leu	Ser	Gln	Val	Leu	Gln
			180					185					190		
Leu	Cys	Leu	Trp	Asp	Gln	Gln	Glu	Ser	Gln	Val	Ser	Cys	Trp	Phe	Gln
		195					200					205			
Lys	Thr	Ile	Arg	Asp	Leu	Gln	Glu	Gln	Ser	Leu	Gly	Ser	Ser	Leu	Ser
	210					215					220				
Asp	Asn	Lys	Glu	Leu	Ile	Arg	Lys	His	Glu	Asp	Leu	Pro	Ser	Lys	Gln
225					230					235					240
Arg	Val	Pro	Ala	Val											
				245											

<210> 65

→ sequences 61 through 64  
missing

09/809,545

7

&lt;400&gt; 65

Met	Thr	Glu	Ser	Val	Val	Cys	Thr	Gly	Ala	Val	Ser	Thr	Val	Lys	Glu
1				5					10					15	
Val	Trp	Glu	Glu	Arg	Ile	Lys	Lys	His	His	Glu	Asp	Val	Lys	Arg	Glu
		20						25					30		
Lys	Glu	Phe	Gln	Gln	Lys	Leu	Val	Arg	Ile	Trp	Glu	Asp	Arg	Val	Ser
		35					40					45			
Leu	Thr	Lys	Leu	Lys	Glu	Lys	Val	Thr	Arg	Glu	Asp	Gly	Arg	Ile	Ile
	50					55					60				
Leu	Arg	Ile	Glu	Lys	Glu	Glu	Trp	Lys	Thr	Leu	Pro	Ser	Ser	Leu	Leu
65				70						75				80	
Lys	Leu	Asn	Gln	Leu	Gln	Glu	Trp	Gln	Leu	His	Arg	Thr	Gly	Leu	Leu
			85					90					95		
Lys	Ile	Pro	Glu	Phe	Ile	Gly	Arg	Phe	Gln	His	Leu	Ile	Gly	Leu	Asp
		100					105						110		
Leu	Ser	Arg	Asn	Thr	Ile	Ser	Glu	Ile	Pro	Pro	Arg	His	Trp	Thr	Xaa
		115					120					125			
His	Leu	Asp	Phe	Lys	Glu	Leu	Ile	Leu	Ser	Tyr	Thr	Lys	Ser		
	130					135					140				

&lt;210&gt; 69

→ Sequences  
66 through 68  
missing

09/809,545 8

<400> 69

Met	Ser	Ser	Ser	His	Leu	Arg	Thr	Arg	Ser	Ala	Arg	Thr	Pro	Gly	Lys
1				5					10					15	
Ile	Pro	Leu	Ile	Pro	Ile	Val	Gly	Asn	Met	Leu	Pro	Ala	Val	Gly	His
			20					25					30		
Leu	Ile	Tyr	Thr	Phe	Ser	Gly	Leu	Thr	His	Tyr	Pro	Lys	Asn	Leu	Leu
		35					40					45			
Thr															

→ sequence 70  
missing

<210> 71



09/809,545

9

&lt;400&gt; 71

Met	Glu	Ile	Asn	Glu	Lys	Leu	Ala	Asp	Ala	Lys	Ser	Glu	Ala	Ala	Met
1				5					10					15	
Glu	Glu	Val	Glu	Ala	Thr	Val	Arg	Ala	Lys	Gln	Lys	Glu	Phe	Thr	Asp
			20					25					30		
Asn	Ile	Asn	Arg	Ala	Phe	Glu	Gln	Gly	Asp	Phe	Glu	Lys	Ala	Lys	Glu
		35					40					45			
Leu	Leu	Thr	Lys	Met	Arg	Tyr	Phe	Ser	Asn	Ile	Glu	Glu	Lys	Ile	Lys
	50					55					60				
Leu	Ser	Lys	Asn	Pro	Leu										
65					70										

&lt;210&gt; 74

→ sequence 72 and 73 missing

09/809,545

10

&lt;400&gt; 74

Met	Ala	Pro	Lys	Lys	Lys	Thr	Leu	Lys	Lys	Asn	Lys	Pro	Glu	Ile	Asn
1				5					10					15	
Glu	Met	Thr	Ile	Ile	Val	Glu	Asp	Ser	Pro	Leu	Asn	Lys	Leu	Asn	Ala
			20					25					30		
Leu	Asn	Gly	Leu	Leu	Gly	Gly	Glu	Asn	Ser	Leu	Ser	Cys	Val	Ser	Phe
		35					40					45			
Glu	Leu	Thr	Asp	Thr	Ser	Tyr	Gly	Pro	Asn	Leu	Leu	Glu	Gly	Leu	Ser
	50					55				60					
Lys	Met	Arg	Gln	Glu	Ser	Phe	Leu	Cys	Asp	Leu	Val	Ile	Gly	Pro	Lys
65					70				75					80	
Pro	Ser	Pro	Leu	Met	Ser	Ile	Ser	Gln	Val	Met	Ala	Ser	Cys	Ser	Glu
				85					90					95	
Ser	Ser	Ile	Ile	Ser	Leu	Lys	Arg	Ser	Ile	Asp	Lys	Lys	Gly	Arg	Pro
			100					105					110		
Gln															

→ Sequence 75 missing

&lt;210&gt; 76

# VERIFICATION SUMMARY

PATENT APPLICATION: US/09/809,545

DATE: 04/04/2001

TIME: 14:11:30

Input Set : A:\SCIOS17ASEQ.TXT

Output Set: N:\CRF3\04042001\I809545.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application No  
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:185 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:376 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:377 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:439 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:499 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
L:500 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
L:502 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
L:503 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
L:504 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
L:520 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:523 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:528 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:529 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:532 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:533 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:540 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:541 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:544 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:545 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:548 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:549 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:550 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:598 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13  
L:600 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13  
L:676 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15  
L:677 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15  
L:680 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15  
L:681 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15  
L:684 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15  
L:822 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16  
L:827 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (17) SEQUENCE:  
L:894 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
L:895 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
L:896 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
L:1050 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
L:1088 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:1135 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24  
L:1136 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24  
L:1137 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24  
L:1406 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28  
L:1466 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29  
L:1467 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29  
L:1469 M:214 E: (33) Seq.# missing, SEQ ID NO:30  
L:1511 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:31  
L:1513 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31  
L:1516 M:214 E: (33) Seq.# missing, SEQ ID NO:32

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/809,545

DATE: 04/04/2001

TIME: 14:11:30

Input Set : A:\SCIOS17ASEQ.TXT

Output Set: N:\CRF3\04042001\I809545.raw

L:1666 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:35  
 L:1717 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37  
 L:1816 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38  
 L:1820 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38  
 L:1823 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38  
 L:1825 M:214 E: (33) Seq.# missing, SEQ ID NO:39  
 L:1846 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40  
 L:1847 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40  
 L:1848 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40  
 L:1849 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40  
 L:2780 M:216 E: (34) Seq.#s missing, SEQ ID NOS: 61 thru 64  
 L:2810 M:216 E: (34) Seq.#s missing, SEQ ID NOS: 66 thru 68  
 L:2825 M:214 E: (33) Seq.# missing, SEQ ID NO:70  
 L:2842 M:216 E: (34) Seq.#s missing, SEQ ID NOS: 72 thru 73  
 L:2865 M:214 E: (33) Seq.# missing, SEQ ID NO:75